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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=16; hr=16; min=14; sec=5; ms=268;]

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Reviewer Comments:

<210> 31

<211> 23

<212> DNA

<213> primer

<400> 31

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23

The above <213> response is invalid, per Sequence Rules. The only valid responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown." "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section; please give the source of the genetic material. Same error in Sequences 32-36 and 40-41.

Application No: 10586823 Version No: 1.0

Input Set:**Output Set:**

Started: 2007-12-31 15:21:50.133
Finished: 2007-12-31 15:21:52.881
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 748 ms
Total Warnings: 26
Total Errors: 8
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
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W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
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Input Set:

Output Set:

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Actual SeqID Count: 42

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 356	Organism is not permitted in <213> in SEQ ID (31)
E 356	Organism is not permitted in <213> in SEQ ID (32)
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SEQUENCE LISTING

<110> Taramino, Graziana
Sakai, Hajime
Meeley, Robert B.
Niu, Xiaomu

<120> ALTERING ROOT STRUCTURE DURING PLANT DEVELOPMENT

<130> BB1545

<140> 10586823

<141> 2007-12-31

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1				5					10					15		

aag	tgc	gtg	cgc	ggc	tgc	gtc	ttc	gcg	ccc	tac	ttc	tgc	cac	gag	cag	96
Lys	Cys	Val	Arg	Gly	Cys	Val	Phe	Ala	Pro	Tyr	Phe	Cys	His	Glu	Gln	
				20				25					30			

ggc	gcg	gcg	cac	ttc	gcc	gcc	atc	cac	aag	gtg	ttc	ggc	gcc	agc	aac	144
Gly	Ala	Ala	His	Phe	Ala	Ala	Ile	His	Lys	Val	Phe	Gly	Ala	Ser	Asn	
				35				40					45			

gtg	tcc	aag	ctg	ctc	gcg	cac	ctg	ccg	ctc	gcc	gac	cgc	gcc	gag	gcc	192
Val	Ser	Lys	Leu	Leu	Ala	His	Leu	Pro	Leu	Ala	Asp	Arg	Ala	Glu	Ala	
				50				55					60			

gcc	gtc	acc	atc	tcc	tac	gag	gcg	cag	gcg	agg	cta	cgc	gac	ccc	atc	240
Ala	Val	Thr	Ile	Ser	Tyr	Glu	Ala	Gln	Ala	Arg	Leu	Arg	Asp	Pro	Ile	
65						70				75				80		

tat	ggc	tgc	gtc	gcc	cac	atc	ttc	gcg	cta	cag	cag	cag	gtg	atg	acc	288
Tyr	Gly	Cys	Val	Ala	His	Ile	Phe	Ala	Leu	Gln	Gln	Gln	Val	Met	Thr	
				85					90					95		

ctg	cag	gcg	cag	ctg	gcg	tcg	ctc	aag	gcg	cag	gcg	gcg	cag	ggg	cag	336
Leu	Gln	Ala	Gln	Leu	Ala	Ser	Leu	Lys	Ala	Gln	Ala	Ala	Gln	Gly	Gln	
				100				105					110			

cag	ggc	gtg	cac	gag	gac	gcc	aag	ggc	tac	gtg	ggc	agc	gcc	gcc	gcg	384
Gln	Gly	Val	His	Glu	Asp	Ala	Lys	Gly	Tyr	Val	Gly					